

#8



1600

RAW SEQUENCE LISTING

DATE: 06/05/2002

PATENT APPLICATION: US/09/641,701A

TIME: 14:57:29

Input Set : A:\195870US0.txt

Output Set: N:\CRF3\06052002\I641701A.raw

3 <110> APPLICANT: KOJIMA, Yoshinao
 4 FUKUMOTO, Satoshi
 5 FURUKAWA, Keiko
 6 OKAJIMA, Tetsuya
 7 FURUKAWA, Koichi
 9 <120> TITLE OF INVENTION: ALPHA 1,4-GALACTOSYLTRANSFERASE AND DNA ENCODING THEREOF
 11 <130> FILE REFERENCE: 195870US0
 13 <140> CURRENT APPLICATION NUMBER: 09/641,701A
 14 <141> CURRENT FILING DATE: 2000-08-21
 16 <150> PRIOR APPLICATION NUMBER: JP 2000-35454
 17 <151> PRIOR FILING DATE: 2000-02-14
 19 <160> NUMBER OF SEQ ID NOS: 2
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1975
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (134)..(1192)
 31 <223> OTHER INFORMATION:
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 39 atctggggat acc atg tcc aag ccc ccc gac ctg ctg cgg ctg ctg 169
 40 Met Ser Lys Pro Pro Asp Leu Leu Arg Leu Leu
 41 1 5 10
 43 cgg ggc gcc cca agg cag cgg gtc tgc acc ctg ttc atc atc ggc ttc 217
 44 Arg Gly Ala Pro Arg Gln Arg Val Cys Thr Leu Phe Ile Ile Gly Phe
 45 15 20 25
 47 aag ttc acg ttt ttc gtc tcc atc atg atc tac tgg cac gtt gtg gga 265
 48 Lys Phe Thr Phe Phe Val Ser Ile Met Ile Tyr Trp His Val Val Gly
 49 30 35 40
 51 gag ccc aag gag aaa ggg cag ctg tat aac ctg cca gca gag atc ccc 313
 52 Glu Pro Lys Glu Lys Gly Gln Leu Tyr Asn Leu Pro Ala Glu Ile Pro
 53 45 50 55 60
 55 tgc ccc acc ttg aca ccc ccc acc cca ccc tcc cac ggc ccc act cca 361
 56 Cys Pro Thr Leu Thr Pro Pro Thr Pro Pro Ser His Gly Pro Thr Pro
 57 65 70 75
 59 ggc aac atc ttc ttc ctg gag act tca gac cgg acc aac ccc aac ttc 409
 60 Gly Asn Ile Phe Phe Leu Glu Thr Ser Asp Arg Thr Asn Pro Asn Phe
 61 80 85 90
 63 ctg ttc atg tgc tcg gtg gag tcg gcc gcc aga act cac ccc gaa tcc 457

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65			95					100					105				
67	cac	gtg	ctg	gtc	ctg	atg	aaa	ggg	ctt	ccg	ggt	ggc	aac	gcc	tct	ctg	505
68	His	Val	Leu	Val	Leu	Met	Lys	Gly	Leu	Pro	Gly	Gly	Asn	Ala	Ser	Leu	
69		110					115				120						
71	ccc	cgg	cac	ctg	ggc	atc	tca	ctt	ctg	agc	tgc	ttc	ccg	aac	gtc	cag	553
72	Pro	Arg	His	Leu	Gly	Ile	Ser	Leu	Leu	Ser	Cys	Phe	Pro	Asn	Val	Gln	
73	125				130					135					140		
75	atg	ctc	ccg	ctg	gac	ctg	cgg	gag	ctg	ttc	cgg	gac	aca	ccc	ctg	gcc	601
76	Met	Leu	Pro	Leu	Asp	Leu	Arg	Glu	Leu	Phe	Arg	Asp	Thr	Pro	Leu	Ala	
77				145					150				155				
79	gac	tgg	tac	gcg	gcc	gtg	cag	ggg	cgc	tgg	gag	ccc	tac	ctg	ctg	ccc	649
80	Asp	Trp	Tyr	Ala	Ala	Val	Gln	Gly	Arg	Trp	Glu	Pro	Tyr	Leu	Leu	Pro	
81			160					165				170					
83	gtg	ctc	tcc	gac	gcc	tcc	agg	atc	gca	ctc	atg	tgg	aag	ttc	ggc	ggc	697
84	Val	Leu	Ser	Asp	Ala	Ser	Arg	Ile	Ala	Leu	Met	Trp	Lys	Phe	Gly	Gly	
85		175				180			185								
87	atc	tac	ctg	gac	acg	gac	ttc	att	gtt	ctc	aag	aac	ctg	cgg	aac	ctg	745
88	Ile	Tyr	Leu	Asp	Thr	Asp	Phe	Ile	Val	Leu	Lys	Asn	Leu	Arg	Asn	Leu	
89		190				195			200								
91	acc	aac	gtg	ctg	ggc	acc	cag	tcc	cgc	tac	gtc	ctc	aac	ggc	gcg	ttc	793
92	Thr	Asn	Val	Leu	Gly	Thr	Gln	Ser	Arg	Tyr	Val	Leu	Asn	Gly	Ala	Phe	
93	205			210					215						220		
95	ctg	gcc	ttc	gag	cgc	cgg	cac	gag	ttc	atg	gcg	ctg	tgc	atg	cgg	gac	841
96	Leu	Ala	Phe	Glu	Arg	Arg	His	Glu	Phe	Met	Ala	Leu	Cys	Met	Arg	Asp	
97			225					230				235					
99	ttc	gtg	gac	cac	tac	aac	ggc	tgg	atc	tgg	ggt	cac	cag	ggc	ccg	cag	889
100	Phe	Val	Asp	His	Tyr	Asn	Gly	Trp	Ile	Trp	Gly	His	Gln	Gly	Pro	Gln	
101			240					245				250					
103	ctg	ctc	acg	cgg	gtc	ttc	aag	aag	tgg	tgt	tcc	atc	cgc	agc	ctg	gcc	937
104	Leu	Leu	Thr	Arg	Val	Phe	Lys	Lys	Trp	Cys	Ser	Ile	Arg	Ser	Leu	Ala	
105			255				260					265					
107	gag	agc	cgc	gcc	tgc	cgc	ggc	gtc	acc	acc	ctg	ccc	cct	gag	gcc	ttc	985
108	Glu	Ser	Arg	Ala	Cys	Arg	Gly	Val	Thr	Thr	Leu	Pro	Pro	Glu	Ala	Phe	
109		270				275					280						
111	tac	ccc	atc	ccc	tgg	cag	gac	tgg	aag	aag	tac	ttt	gag	gac	atc	aac	1033
112	Tyr	Pro	Ile	Pro	Trp	Gln	Asp	Trp	Lys	Lys	Tyr	Phe	Glu	Asp	Ile	Asn	
113	285				290				295						300		
115	ccg	gag	gag	ctg	ccg	cgg	ctg	ctc	agt	gcc	acc	tat	gct	gtc	cac	gtg	1081
116	Pro	Glu	Glu	Leu	Pro	Arg	Leu	Leu	Ser	Ala	Thr	Tyr	Ala	Val	His	Val	
117			305					310				315					
119	tgg	aac	aag	aag	agc	cag	ggc	acg	cgg	ttc	gag	gcc	acg	tcc	agg	gca	1129
120	Trp	Asn	Lys	Lys	Ser	Gln	Gly	Thr	Arg	Phe	Glu	Ala	Thr	Ser	Arg	Ala	
121			320					325				330					
123	ctg	ctg	gcc	cag	ctg	cat	gcc	cgc	tac	tgc	ccc	acg	acg	cac	gag	gcc	1177
124	Leu	Leu	Ala	Gln	Leu	His	Ala	Arg	Tyr	Cys	Pro	Thr	Thr	His	Glu	Ala	
125			335				340					345					
127	atg	aaa	atg	tac	ttg	tgaggggccc	gccaggtcac	ctccccaacc	tgctcctgat								1232
128	Met	Lys	Met	Tyr	Leu												

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135 tgtggacacc ccgaggacag tgtcctgtct cgaggcaggg ctgacacatg gtgccatagc 1412
137 cagcggaggg cgctcagtga gtgccccggg ccttctagac aacaggcagg aaggatgaac 1472
139 ctgagggcac ccccagggtg tgcggaaagc caggcagttg ggacagaggt gcccacgagg 1532
141 gcagaggccg gtgctaaggg gatggggaag aagggacaag attcccagag aggagaggag 1592
143 gctgttggtg ggaaagtggc agggctgggg gagaccagc cccaagggtc cggggcggag 1652
145 gatgctttgt tcttttctgg ttttggttcc tctttcgcgg ggggtggggg aggtcaacag 1712
147 ggactgagtg gggcagaggc ccagaagtgc cagcctgggg agccgtttgg gggcagcccc 1772
149 ttctgcccac cccatccttc ttctctcca gagatgccag gggggcgtgt atgctctgcc 1832
151 ccttccctca gacaggggct ggggtggggag gctctttagg ctgaggagaa gcattttaaa 1892
153 gaaaccccca cctgcccgc cgcattataa acacaggaga ataatcaata gaataaaaagt 1952
155 gaccgactgt caaaaaaaaa aaa 1975
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159 <211> LENGTH: 353
160 <212> TYPE: PRT
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173 Phe Val Ser Ile Met Ile Tyr Trp His Val Val Gly Glu Pro Lys Glu
174 35 40 45
177 Lys Gly Gln Leu Tyr Asn Leu Pro Ala Glu Ile Pro Cys Pro Thr Leu
178 50 55 60
181 Thr Pro Pro Thr Pro Pro Ser His Gly Pro Thr Pro Gly Asn Ile Phe
182 65 70 75 80
185 Phe Leu Glu Thr Ser Asp Arg Thr Asn Pro Asn Phe Leu Phe Met Cys
186 85 90 95
189 Ser Val Glu Ser Ala Ala Arg Thr His Pro Glu Ser His Val Leu Val
190 100 105 110
193 Leu Met Lys Gly Leu Pro Gly Gly Asn Ala Ser Leu Pro Arg His Leu
194 115 120 125
197 Gly Ile Ser Leu Leu Ser Cys Phe Pro Asn Val Gln Met Leu Pro Leu
198 130 135 140
201 Asp Leu Arg Glu Leu Phe Arg Asp Thr Pro Leu Ala Asp Trp Tyr Ala
202 145 150 155 160
205 Ala Val Gln Gly Arg Trp Glu Pro Tyr Leu Leu Pro Val Leu Ser Asp
206 165 170 175
209 Ala Ser Arg Ile Ala Leu Met Trp Lys Phe Gly Gly Ile Tyr Leu Asp
210 180 185 190
213 Thr Asp Phe Ile Val Leu Lys Asn Leu Arg Asn Leu Thr Asn Val Leu
214 195 200 205
217 Gly Thr Gln Ser Arg Tyr Val Leu Asn Gly Ala Phe Leu Ala Phe Glu
218 210 215 220
221 Arg Arg His Glu Phe Met Ala Leu Cys Met Arg Asp Phe Val Asp His
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234                275                280                285
237 Trp Gln Asp Trp Lys Lys Tyr Phe Glu Asp Ile Asn Pro Glu Glu Leu
238                290                295                300
241 Pro Arg Leu Leu Ser Ala Thr Tyr Ala Val His Val Trp Asn Lys Lys
242 305                310                315                320
245 Ser Gln Gly Thr Arg Phe Glu Ala Thr Ser Arg Ala Leu Leu Ala Gln
246                325                330                335
249 Leu His Ala Arg Tyr Cys Pro Thr Thr His Glu Ala Met Lys Met Tyr
250                340                345                350
253 Leu

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VERIFICATION SUMMARY

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